

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Freeman, Gordon J.
Nadler, Lee M.
Gray, Gary S.

10

(ii) TITLE OF INVENTION: Novel CTLA4/CD28 Ligands and
Uses Therefor

(iii) NUMBER OF SEQUENCES: 31

15

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Boston
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20 (E) COUNTRY: USA
(F) ZIP: 02109

20

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

35

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/280,757; 08/101,624; 08/109,393;
08/147,773
(B) FILING DATE: 26-JUL-1994; 26-JUL-1993; 19-AUG-1993; 03-NOV-
1993

40

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: RPI-004CP3

45

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1120 base pairs
5 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 107..1093

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	CACAGGGTGA AAGCTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
20	GAGTGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAAGCA GCCAAA ATG GAT CCC Met Asp Pro	115
	1	
25	CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu 5 10 15	163
30	CTC TCT GGT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr 20 25 30 35	211
	GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser 40 45 50	259
35	GAG CTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu 55 60 65	307
40	GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met 70 75 80	355
45	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn 85 90 95	403
50	CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys 100 105 110 115	451
55	AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser 120 125 130	499

	GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile 135 140 145	547
5	ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr 150 155 160	595
10	CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr 165 170 175	643
15	ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu 180 185 190 195	691
20	CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr 200 205 210	739
25	AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu 215 220 225	787
30	TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro 230 235 240	835
35	GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys 245 250 255	883
40	GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Arg 260 265 270 275	931
45	CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu 280 285 290	979
50	AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser 295 300 305	1027
	GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp 310 315 320	1075
	AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAAA Lys Ser Asp Thr Cys Phe 325	1120

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
1 5 10 15

15 Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
20 35 40 45

20 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
50 55 60

25 Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65 70 75 80

25 Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
85 90 95

30 Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
100 105 110

35 His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
115 120 125

35 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
130 135 140

40 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145 150 155 160

40 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
165 170 175

45 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
180 185 190

50 Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
195 200 205

50 Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210 215 220

55 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225 230 235 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245 250 255

5 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
260 265 270

Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
275 280 285

10 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290 295 300

15 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

20 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 TAATACGACT CACTATAGGG

20

35 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

50 TAAGGTTCT TCACAAAG

18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

55

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: oligonucleotide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTGGTAGGT ATGGAAGATC C

21

(2) INFORMATION FOR SEQ ID NO:6:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: oligonucleotide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCGAATCA TTCCTGTGGG C

21

30 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: oligonucleotide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGCCCACA GGAATGATTC G

21

45 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: oligonucleotide

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 CTCTCAAAAC CAAAGCCTGA G

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 15 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 TTAGGTCACA GCAGAAGCAG C

21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 30 (ii) MOLECULE TYPE: oligonucleotide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTGGAAACT GACAAGACGC G

21

(2) INFORMATION FOR SEQ ID NO:11:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: oligonucleotide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTCAGGCTTT GGTTTGAGA G

21

(2) INFORMATION FOR SEQ ID NO:12:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 CACTCTCTTC CCTCTCCATT G

21

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

30 GACAAGCTGA TGGAAACGTC G

21

(2) INFORMATION FOR SEQ ID NO:14:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

45 CAATGGAGAG GGAAGAGAGT G

21

(2) INFORMATION FOR SEQ ID NO:15:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: oligonucleotide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTTAGAGCA CA

12

10 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCTAAAG

8

25 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Tyr Met Gly Arg Thr Ser Phe Asp

5

40

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

SEQUENCE DESCRIPTION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Ser Gln Asp Asn Val Thr Glu Lys Tyr Asp Val Ser
5 10

5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Trp Lys Trp Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys
20 5 10 15

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: oligonucleotide

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGCCCATGG CTTCAGA

17

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: oligonucleotide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCCAAATGG ATCCCCA

17

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 111..1040

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

20	CCCACCGCGTC CGGGAGCAAG CAGACCGCGTA AGAGTGGCTC CTGTAGGCAG CACGGACTTG	60
25	AACAAACCAGA CTCCTGTAGA CGTGTTCAG AACTTACGGA AGCACCCACG ATG GAC Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu 5 10 15	116 Met Asp 1
30	CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly 20 25 30	212
35	ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu 35 40 45 50	260
40	AGT GAG CTG GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr 55 60 65	308
45	GAG CAC TAT TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr 70 75 80	356
50	CTG GGC CGC ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His 85 90 95	404
55	AAT GTT CAG ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys 100 105 110	452
55	AAG CCA CCC ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu 115 120 125 130	500

	TCA GTG ATC GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn 135 140 145	548
5	GTA ACA GGA AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly 150 155 160	596
10	CAC CCG AAA CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn 165 170 175	644
15	GAG TAT GGT GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu 180 185 190	692
20	TTC AGT ATC TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG Phe Ser Ile Ser Asn Ser Leu Ser Phe Pro Asp Gly Val Trp 195 200 205 210	740
25	CAT ATG ACC GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser 215 220 225	788
30	TCC AAA CCT CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr 230 235 240	836
35	TGG AAG GAG ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met 245 250 255	884
40	CTG CTC ATC ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro 260 265 270	932
45	AGC AAC ACA GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu 275 280 285 290	980
	ACT ATC AAC CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA Thr Ile Asn Leu Lys Glu Leu Pro Gln Ile Ala Ser Ala Lys Pro 295 300 305	1028
	AAT GCA GAG TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT Asn Ala Glu	1077
50	TTGCCTGAAA TAAGAAGTGC AGAGTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA AAGAAC	1137
		1163

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr
1 5 10 15

15 Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe
20 25 30

Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile
20 35 40 45

25 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val
50 55 60

Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala
25 65 70 75 80

30 Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg
85 90 95

35 Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile
100 105 110

Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr
35 115 120 125

40 Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
130 135 140

Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
40 145 150 155 160

Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
165 170 175

45 Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
180 185 190

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
50 195 200 205

50 Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
210 215 220

55 Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
225 230 235 240

Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
245 250 255

5 Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
260 265 270

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
275 280 285

10 Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
290 295 300

Lys Pro Asn Ala Glu
15 305

(2) INFORMATION FOR SEQ ID NO:24:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: oligonucleotide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACATAAGCCT GAGTGAGCTG G

21

35 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGATGAGCA GCATCACAAAG G

21

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5 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15 TGGTCGAGTG AGTCCGAATA C

21

20 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: oligonucleotide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACGAGTAGT AACATACAGT G

21

35 (2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

50

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: Homo sapien
(F) TISSUE TYPE: lymphoid
(G) CELL TYPE: B cell
(H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

10 (A) LIBRARY: cDNA in pCDM8 vector
(B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

15 (A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

20 (A) NAME/KEY: Open reading frame (translated region)
(B) LOCATION: 318 to 1181 bp
(C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

25 (A) NAME/KEY: Alternate polyadenylation signal
(B) LOCATION: 1474 to 1479 bp
(C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

30 (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE

35 WHITMAN, JAMES F.
NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells

40 (C) JOURNAL: The Journal of Immunology

(D) VOLUME: 143

(E) ISSUE: 8

(F) PAGES: 2714-2722

45 (G) DATE: 15-OCT-1989

(H) RELEVANT RESIDUES In SEQ ID NO:28: FROM 1 TO 1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

50 CCAAAGAAAA AGTGATTGT CATTGCTTA TAGACTGTA GAAGAGAACCA TCTCAGAAAGT 60
GGAGTCTTAC CCTGAAATCA AAGGATTAA AGAAAAAGTG GAATTTTCT TCAGCAAGCT 120
55 GTGAAACTAA ATCCACAAACC TTTGGAGACC CAGAACACC CTCCAATCTC TGTGTGTTT 180

GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTACATCAGC CCTGCCTGTT 240
TTGCACCTGG GAAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTGAC 300
5 CCTAAGCATC TGAAGGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
-30 -25

10 AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
-20 -15 -10

15 TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
-5 1 5 10

20 GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 497
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
15 20 25

25 CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG 545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
30 35 40

30 ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC 593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
45 50 55

35 TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA 641
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
60 65 70

40 TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC 689
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
75 80 85 90

45 GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT 737
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
95 100 105

50 GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT 785
Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
110 115 120

55

ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC 833
Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His
125 130 135

5 CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA 881
Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr
140 145 150

10 GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG 929
Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu
155 160 165 170

15 GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT 977
Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr
175 180 185

20 GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA 1025
Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln
190 195 200

25 GAG CAT TTT CCT GAT AAC CTG CTC CCA TCC TGG GCC ATT ACC TTA ATC 1073
Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile
205 210 215

30 TCA GTA AAT GGA ATT TTT GTG ATA TGC TGC CTG ACC TAC TGC TTT GCC 1121
Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala
220 225 230

35 CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA AGT 1169
Pro Arg Cys Arg Glu Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser
235 240 245 250

40 GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA 1221
Val Arg Pro Val

45 GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC 1281

CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAAACCT CTTTCAGATT 1341

50 AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTGCT 1401

TAATGTAACC TCTTCTTTG CCATGTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461

55

AATTCATTAT CTATTAACCA CTAATTTGAG
1491

5

(3) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 288 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

15 (A) DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein

20 (ix) FEATURE:

20 (A) NAME/KEY: signal sequence
(B) LOCATION: -34 to -1
(C) IDENTIFICATION METHOD: amino terminal sequencing of
soluble protein

25 (D) OTHER INFORMATION: hydrophobic

30 (ix) FEATURE:

30 (A) NAME/KEY: extracellular domain
(B) LOCATION: 1 to 208
(C) IDENTIFICATION METHOD: similarity with known
sequence

35 (ix) FEATURE:

35 (A) NAME/KEY: transmembrane domain
(B) LOCATION: 209 to 235
(C) IDENTIFICATION METHOD: similarity with known
sequence

40

(ix) FEATURE:

45 (A) NAME/KEY: intracellular domain
(B) LOCATION: 236 to 254
(C) IDENTIFICATION METHOD: similarity with known
sequence

50

5 (ix) FEATURE:

(A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 19 to 21
(C) IDENTIFICATION METHOD: similarity with known
sequence

10 (ix) FEATURE:

(A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 55 to 57
(C) IDENTIFICATION METHOD: similarity with known
sequence

15

(ix) FEATURE:

20 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 64 to 66
(C) IDENTIFICATION METHOD: similarity with known
sequence

25

(ix) FEATURE:

(A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 152 to 154
(C) IDENTIFICATION METHOD: similarity with known
sequence

30

(ix) FEATURE:

35 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 173 to 175
(C) IDENTIFICATION METHOD: similarity with known
sequence

40

(ix) FEATURE:

45 (A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 177 to 179
(C) IDENTIFICATION METHOD: similarity with known
sequence

50

(ix) FEATURE:

(A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 192 to 194
(C) IDENTIFICATION METHOD: similarity with known
sequence

55

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5 (ix) FEATURE:

(A) NAME/KEY: N-linked glycosylation
(B) LOCATION: 198 to 200
(C) IDENTIFICATION METHOD: similarity with known sequence

10 (ix) FEATURE:

(A) NAME/KEY: Ig V-set domain
(B) LOCATION: 1 to 104
(C) IDENTIFICATION METHOD: similarity with known sequence

15 (ix) FEATURE:

20 (A) NAME/KEY: Ig C-set domain
(B) LOCATION: 105 to 202
(C) IDENTIFICATION METHOD: similarity with known sequence

25 (x) PUBLICATION INFORMATION:

(A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.

30
35 (B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
(C) JOURNAL: The Journal of Immunology
(D) VOLUME: 143
(E) ISSUE: 8
(F) PAGES: 2714-2722
40 (G) DATE: 15-OCT-1989
(H) RELEVANT RESIDUES IN SEQUENCE ID NO:29: From -26 to 262

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

DOCUMENT RELEASED BY GOVERNMENT CONTRACTOR

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
-30 -25 -20

Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
5 -15 -10 -5

Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
-1 1 5 10

10 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
15 20 25 30

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
35 40 45

15 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
50 55 60

20 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
65 70 75

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
80 85 90

25 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
95 100 105 110

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
115 120 125

30 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
130 135 140

35 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
145 150 155

Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
160 165 170

40 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
175 180 185 190

45 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
195 200 205

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
210 215 220

50 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
225 230 235

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
240 245 250

(4) INFORMATION FOR SEQ ID NO:30:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 10 (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: cDNA to mRNA

15 (iii) HYPOTHETICAL: no

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus
- (D) DEVELOPMENTAL STAGE: germ line
- 20 (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B lymphocyte
- (H) CELL LINE: 70Z and A20

25 (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA in pCDM8 vector
- (B) CLONE: B7 #'s 1 and 29

30 (ix) FEATURE:

- (A) NAME/KEY: translated region
- (B) LOCATION: 249 to 1166 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

35 (ix) FEATURE:

- (A) NAME/KEY: Alternate ATG initiation codons
- (B) LOCATION: 225 to 227 and 270 to 272
- (C) IDENTIFICATION METHOD: similarity to other pattern

09425546-102290

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTTTTC TCAGGTTGTG AAACTCAACC 60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
5 TGGATGCCAT CCAGGCTTCT TTTCTACAT CTCTGTTCT CGATTTTGT GAGCCTAGGA 180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTCCC CATCATGTT CTCAAAGCAT 240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
10 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
-35 -30 -25
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
Lys Phe Pro Cys Pro Arg Leu Ile Leu Phe Val Leu Leu Ile Arg
15 -20 -15 -10
CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
-5 -1 1 5
20 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434
Lys Asp Lys Val Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
10 15 20 25
25 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
30 35 40
TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
45 50 55
35 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578
Thr Leu Tyr Asp Asn Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
60 65 70
CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626
Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
75 80 85
40 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674
Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
90 95 100 105
45 GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA 722
Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
110 115 120
50 GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT 770
Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
125 130 135
55 CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG 818
Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
140 145 150

ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA 866
Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
155 160 165

5 CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA 914
Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys
170 175 180 185

10 TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA 962
Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro
190 195 200

15 GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA 1010
Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
205 210 215

20 TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC 1058
Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
220 225 230

25 TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA 1106
Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu
235 240 245

30 ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG 1154
Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln
250 255 260 265

35 ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG 1206
Thr Val Phe Leu

GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTCGG ACAACTTGAC 1266

40 ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG 1326
CTACGGCAA GTTGCTGGG CCTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC 1386
ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA 1446
GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTGGTTG 1506
GTGTCTGTGG GAGGCCTGCC CTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG 1566

45 GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1626
GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1686
AGAGTATTGA GCAAAAAAAA AAAAAAAA
50 1716

(5) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

10 (A) DESCRIPTION: B lymphocyte activation antigen; Ig superfamily member; T cell costimulatory signal via activation of CD28 pathways, binds to CD28⁺ T cells, transmembrane protein

15 (ix) FEATURE:

20 (A) NAME/KEY: signal sequence
(B) LOCATION: -37 to -1
(C) IDENTIFICATION METHOD: similarity with known sequence
(D) OTHER INFORMATION: hydrophobic

25 (ix) FEATURE:

30 (A) NAME/KEY: extracellular domain
(B) LOCATION: 1 to 210
(C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

35 (A) NAME/KEY: transmembrane domain
(B) LOCATION: 211 to 235
(C) IDENTIFICATION METHOD: similarity with known sequence

40 (ix) FEATURE:

45 (A) NAME/KEY: intracellular (cytoplasmic) domain
(B) LOCATION: 236 to 269
(C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

50 (A) NAME/KEY: Ig V-set domain
(B) LOCATION: 1 to 105
(C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

5 (A) NAME/KEY: Ig C-set domain
(B) LOCATION: 106 to 199
(C) IDENTIFICATION METHOD: similarity with known
sequence

10 (x) PUBLICATION INFORMATION:

10 (A) AUTHORS: FREEMAN, GORDON J.
GRAY, GARY S.
GIMMI, CLAUDE D.
LOMBARD, DAVID B.
15 ZHOU, LIANG-JI
WHITE, MICHAEL
FINGEROTH, JOYCE D.
GRIBBEN, JOHN G.
NADLER, LEE M.
20 (B) TITLE: Structure, Expression, and T Cell Costimulatory
Activity Of The Murine Homologue Of The Human B
Lymphocyte Activation Antigen B7
(C) JOURNAL: Journal of Experimental Medicine
25 (D) VOLUME:
(E) ISSUE:
(F) PAGES:
(G) DATE: IN PRESS
(H) RELEVANT RESIDUES IN SEQUENCE ID NO:31: From -37 to 269
30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
-35 -30 -25

40 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
-20 -15 -10

45 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
-5 -1 1 5 10

50 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
15 20 25

55 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
30 35 40

60 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
45 50 55

65 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
70 75

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
80 85 90

5 Tyr Gly Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
95 100 105

Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
110 115 120

10 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
125 130 135

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
140 145 150 155

15 Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
160 165 170

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
20 175 180 185

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
190 195 200

25 Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
205 210 215

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
220 225 230 235

30 Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
240 245 250

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
35 255 260 265

Phe Leu

40